

# RAW SEQUENCE LISTING

EFS

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/817,483A  
Source: 1FW16  
Date Processed by STIC: 2/12/07

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 02/12/2007

PATENT APPLICATION: US/10/817,483A

TIME: 14:20:33

Input Set : N:\efs\02\_12\_07\10817483a\_efs\0803R\_AMDSEQLIST.TXT

Output Set: N:\CRF4\02122007\J817483A.raw

4 <110> APPLICANT: Habben, Jeffrey E.  
 5 Zinselmeier, Christopher  
 6 Tomes, Dwight  
 7 Abbitt, Shane  
 8 Helentjaris, Timothy G.  
 9 Niu, Xiaomu  
 13 <120> TITLE OF INVENTION: Modulation of Cytokinin Activity in  
 14 Plants  
 16 <130> FILE REFERENCE: 0803R  
 18 <140> CURRENT APPLICATION NUMBER: US 10/817,483A  
 19 <141> CURRENT FILING DATE: 2004-04-02  
 21 <150> PRIOR APPLICATION NUMBER: US 60/460,718  
 22 <151> PRIOR FILING DATE: 2003-04-04  
 24 <150> PRIOR APPLICATION NUMBER: US 09/545,334  
 25 <151> PRIOR FILING DATE: 2000-04-07  
 27 <150> PRIOR APPLICATION NUMBER: US 60/129,844  
 28 <151> PRIOR FILING DATE: 1999-04-16  
 30 <160> NUMBER OF SEQ ID NOS: 43  
 32 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 34 <210> SEQ ID NO: 1  
 35 <211> LENGTH: 1919  
 36 <212> TYPE: DNA  
 37 <213> ORGANISM: Agrobacterium tumefaciens  
 39 <220> FEATURE:  
 40 <221> NAME/KEY: CDS  
 41 <222> LOCATION: (690)...(1411)  
 42 <223> OTHER INFORMATION: ipt  
 44 <400> SEQUENCE: 1  
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 46 aataacgaat gtaatggcgt agaaatatgt attttattgt atttatcttt cactatgttg 120  
 47 aagtttgcaa taatatgcta atgtaaaatt aaaaaattat gtactgccgc atttgttcaa 180  
 48 atggcgccgt tatttcaaaa atatctttga ttttgttacg aggacaacga ctgcaggaag 240  
 49 taaataaaaag acgctgttgt taagaaaattg ctatcatatg tgcccagcta tagggccatt 300  
 50 taagtccaat tgtgaaatag ccgcccttat tttgacgtct catcaaatca aatattaaaa 360  
 51 aatatctcac tctgtcgcca gcaatgatgt aataaccgca gaaaagtga agtaaatcgc 420  
 52 ggaaaaacgt cgccgagtgg catgaatagc ggccctcgta ttgctgattt agtcagcttt 480  
 53 atttgactta agggtgccct cgtttagtgac aaattgcttt caaggagaca gccatgcccc 540  
 54 acactttgtt gaaaaacaag ttgccttttg ggaagaacct aaagccactt gctcttcaag 600  
 55 gaggaatatc gaggaagaga atataacagc ctctggtaca gacttctctt gtgcaaaaat 660  
 56 caatttgtat tcaacatatc gcaagaccg atg gat cta cgt cta att ttc ggt 713  
 57 Met Asp Leu Arg Leu Ile Phe Gly  
 58 1 5  
 60 cca act tgc aca gga aag aca tcg act gcg ata gct ctt gcc cag cag 761

*see p. 6*

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62      10                      15                      20
64 act ggc ctc cca gtc ctc tcg ctc gat cgc gtc caa tgc tgt cct caa      809
65 Thr Gly Leu Pro Val Leu Ser Leu Asp Arg Val Gln Cys Cys Pro Gln
66 25                      30                      35                      40
68 cta tca acc gga agc ggg cga cca aca gtg gaa gaa ctg aaa gga acg      857
69 Leu Ser Thr Gly Ser Gly Arg Pro Thr Val Glu Glu Leu Lys Gly Thr
70                      45                      50                      55
72 act cgt ctg tac ctt gat gat cgc cct ttg gta aag ggt atc att aca      905
73 Thr Arg Leu Tyr Leu Asp Asp Arg Pro Leu Val Lys Gly Ile Ile Thr
74                      60                      65                      70
76 gcc aag caa gct cat gaa cgg ctc att gcg gag gtg cac aat cac gag      953
77 Ala Lys Gln Ala His Glu Arg Leu Ile Ala Glu Val His Asn His Glu
78                      75                      80                      85
80 gcc aaa ggc ggg ctt att ctt gag gga gga tct atc tcg ttg ctc agg      1001
81 Ala Lys Gly Gly Leu Ile Leu Glu Gly Gly Ser Ile Ser Leu Leu Arg
82 90                      95                      100
84 tgc atg gcg caa agt cgt tat tgg aac gcg gat ttt cgt tgg cat att      1049
85 Cys Met Ala Gln Ser Arg Tyr Trp Asn Ala Asp Phe Arg Trp His Ile
86 105                      110                      115                      120
88 att cgc aac gag tta gca gac gag gag agc ttc atg agc gtg gcc aag      1097
89 Ile Arg Asn Glu Leu Ala Asp Glu Glu Ser Phe Met Ser Val Ala Lys
90                      125                      130                      135
92 acc aga gtt aag cag atg tta cgc ccc tct gca ggt ctt tct att atc      1145
93 Thr Arg Val Lys Gln Met Leu Arg Pro Ser Ala Gly Leu Ser Ile Ile
94                      140                      145                      150
96 caa gag ttg gtt caa ctt tgg agg gag cct cgg ctg agg ccc ata ctg      1193
97 Gln Glu Leu Val Gln Leu Trp Arg Glu Pro Arg Leu Arg Pro Ile Leu
98                      155                      160                      165
100 gaa ggg atc gat gga tat cga tat gcc ctg cta ttt gct acc cag aac      1241
101 Glu Gly Ile Asp Gly Tyr Arg Tyr Ala Leu Leu Phe Ala Thr Gln Asn
102 170                      175                      180
104 cag atc acg ccc gat atg cta ttg cag ctc gac gca gat atg gag aat      1289
105 Gln Ile Thr Pro Asp Met Leu Leu Gln Leu Asp Ala Asp Met Glu Asn
106 185                      190                      195                      200
108 aaa ttg att cac ggt atc gct cag gag ttt cta atc cat gcg cgt cga      1337
109 Lys Leu Ile His Gly Ile Ala Gln Glu Phe Leu Ile His Ala Arg Arg
110                      205                      210                      215
112 cag gaa cag aaa ttc cct ttg gtg ggc gcg aca gct gtc gaa gcg ttt      1385
113 Gln Glu Gln Lys Phe Pro Leu Val Gly Ala Thr Ala Val Glu Ala Phe
114                      220                      225                      230
116 gaa gga cca cca ttt cga atg tga ta gattgcacca gttttgtttc      1431
117 Glu Gly Pro Pro Phe Arg Met *
118                      235
120 agacttgctg ctatttgaat aagatgttcg ttctttgttg tgttggtgtg ttgtgataga 1491
121 ggcaagtggg ttgaaacttg tttttactgg tttattttca gtctcttgga cgatgtttta 1551
122 caaatataat attgtgaaaa ttgtggtttt atattcgtag aacgaaataa atggtaagta 1611
123 tagccgttat caaaaattag caaaaattgt taaaggttct tttatgcggt gaggtgtcgc 1671
124 acttttcatc attgtcgcgt aaggagttac ggatatccat aactgtaaaa acgcccaga 1731

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125 atttacgggt ggtgcattta gtttgccgtt caacatgatt ttggcaatag ttggtaacca 1791  
 126 agcactagcc aaccgttcga taatcactta atcgatggaa ccgttcagct ttccttcgtg 1851  
 127 aggctgctct tgatgatgag ctgccgtcta gtttttataa cgccgggtta cgcattatag 1911  
 128 acaagctt 1919

130 &lt;210&gt; SEQ ID NO: 2

131 &lt;211&gt; LENGTH: 239

132 &lt;212&gt; TYPE: PRT

133 &lt;213&gt; ORGANISM: Agrobacterium tumefaciens

135 &lt;400&gt; SEQUENCE: 2

136 Met Asp Leu Arg Leu Ile Phe Gly Pro Thr Cys Thr Gly Lys Thr Ser  
 137 1 5 10 15  
 138 Thr Ala Ile Ala Leu Ala Gln Gln Thr Gly Leu Pro Val Leu Ser Leu  
 139 20 25 30  
 140 Asp Arg Val Gln Cys Cys Pro Gln Leu Ser Thr Gly Ser Gly Arg Pro  
 141 35 40 45  
 142 Thr Val Glu Glu Leu Lys Gly Thr Thr Arg Leu Tyr Leu Asp Asp Arg  
 143 50 55 60  
 144 Pro Leu Val Lys Gly Ile Ile Thr Ala Lys Gln Ala His Glu Arg Leu  
 145 65 70 75 80  
 146 Ile Ala Glu Val His Asn His Glu Ala Lys Gly Gly Leu Ile Leu Glu  
 147 85 90 95  
 148 Gly Gly Ser Ile Ser Leu Leu Arg Cys Met Ala Gln Ser Arg Tyr Trp  
 149 100 105 110  
 150 Asn Ala Asp Phe Arg Trp His Ile Ile Arg Asn Glu Leu Ala Asp Glu  
 151 115 120 125  
 152 Glu Ser Phe Met Ser Val Ala Lys Thr Arg Val Lys Gln Met Leu Arg  
 153 130 135 140  
 154 Pro Ser Ala Gly Leu Ser Ile Ile Gln Glu Leu Val Gln Leu Trp Arg  
 155 145 150 155 160  
 156 Glu Pro Arg Leu Arg Pro Ile Leu Glu Gly Ile Asp Gly Tyr Arg Tyr  
 157 165 170 175  
 158 Ala Leu Leu Phe Ala Thr Gln Asn Gln Ile Thr Pro Asp Met Leu Leu  
 159 180 185 190  
 160 Gln Leu Asp Ala Asp Met Glu Asn Lys Leu Ile His Gly Ile Ala Gln  
 161 195 200 205  
 162 Glu Phe Leu Ile His Ala Arg Arg Gln Glu Gln Lys Phe Pro Leu Val  
 163 210 215 220  
 164 Gly Ala Thr Ala Val Glu Ala Phe Glu Gly Pro Pro Phe Arg Met  
 165 225 230 235

168 &lt;210&gt; SEQ ID NO: 3

169 &lt;211&gt; LENGTH: 2085

170 &lt;212&gt; TYPE: DNA

171 &lt;213&gt; ORGANISM: Zea mays

173 &lt;220&gt; FEATURE:

174 &lt;221&gt; NAME/KEY: promoter

175 &lt;222&gt; LOCATION: (1)...(2085)

176 &lt;223&gt; OTHER INFORMATION: zag2.1

178 &lt;400&gt; SEQUENCE: 3

179 agcttcgtgt gttccttcga tcggtcacag ttgattcct gctcaccaca tatttttgcc 60

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181 ttaataactc ttatatcttc tactataaca tcaaaataag acgtagtgtg gtggatatgt 180
182 tgtctctaata ttagcagcag gtcttgagtt tgattcacaa ttcttgcaga tttatttttt 240
183 gagccataac agggatgagg gcaaaatagg aaatgaacga catgttacct ttaccgcctt 300
184 aataagtagt agagatatcc agtttatatc taattattat tatataaaat gcactgcaca 360
185 tataattacta ttaccagttt tcttggacat gcacagcaga aaacacgcac acgcagagag 420
186 gaaaaggaga ggccataaac caaaaggcct taagaatata tgtaaagata tgtctaaatg 480
187 gctatatctg gttaagcaag ataacagggc tctggtcatc agtagtagtg gccttttgcc 540
188 cttgcccctc atctctctca cacctctctt ttctcagcct tgcttccgat cgatggatcc 600
189 catcccactg ccatagtgcc atcctttctt tcccttgccg gcattgccta gccggccggc 660
190 cggcctgcta ttaaacact ttacccccct tctcgttcac gctcgacgca gctccctttt 720
191 ccttgcttgc ttattgcaag tctctgcaag aacctgctag agaggaacaa ggtagaatag 780
192 tatcgctttt tccatctaga ggttatctct ttttacatga aaaattttcag ccgtattttc 840
193 gttctccata tatcagtcct gcgataatat aaatacgcgc gtcttgtgtg atccggcata 900
194 tgtatagtct ctactaactg atcgagatcg ctctcgtttg tactttctcc ctttgaggaa 960
195 agagttcccc tttttctgtg cttcaaattc ttgtaaggaa aacctgcct gcctgccagc 1020
196 ttcttctgct acttgatga tgattcttat ttgcttactt gatttccgtt tttttttctt 1080
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198 tttggaaggt ttcaactctt tgtatacgat gaggtttctg cccctagtag cagatccgcg 1200
199 cagactaga tgtttgagga aaagaaaagg gcaagacgct atatatatat gcagcacgca 1260
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204 tcattgccgg tttgttggtt tttcgtgttt ttttagcttc ttgtcccca tttatattcg 1560
205 cgcctaatac acgagcccggt agatcttggt ttcttgtggc tggttttgtt ggatctcgat 1620
206 ctcggttacg tttacatgag tcttgctgcc taacatacat ctgtgttctt tttctaggct 1680
207 gcgagaaact taactgatcg agtctgtctg gcaggcatcg atctatccag tcgtcagttc 1740
208 gtcacatccg ctttttcgta tatatcatct tcagattttg tccatctgtc aaatcatgga 1800
209 aaatctgtcg cttttgcttg tattctcttc tgttattcct gctgcctccg gcggaccaat 1860
210 tcttgaaatcg acccggttct ctattccctt ttgttagaca gccc aaatcg cttgctcgat 1920
211 cgtagtgtac tgtactactg cggctagcta gatcttccaa gctagctata gttcgccggt 1980
212 ccctttgatc tgcttcacag aacatatata acacttgaac tcttttacgc ttatgagaaa 2040
213 acttgctgct tgctgctttc agctggtatc gtcgccagcg gatcc 2085

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215 &lt;210&gt; SEQ ID NO: 4

216 &lt;211&gt; LENGTH: 344

217 &lt;212&gt; TYPE: DNA

218 &lt;213&gt; ORGANISM: Cauliflower mosaic virus

220 &lt;220&gt; FEATURE:

221 &lt;221&gt; NAME/KEY: enhancer

222 &lt;222&gt; LOCATION: (1)...(344)

223 &lt;223&gt; OTHER INFORMATION: CaMV35s

225 &lt;400&gt; SEQUENCE: 4

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228 acctcctcgg attccattgc ccagctatct gtcacttcat caaaaggaca gtagaaaagg 180
229 aagggtggcac ctacaaatgc catcattgct ataaaggaaa ggctatcgtt caagatgcct 240
230 ctgccgacag tgggtcccaa gatggacccc caccacagag gagcatcgtg gaaaaaagaag 300
231 acgttccaac cagctcttca aagcaagtgg attgatgtga tgct 344

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Output Set: N:\CRF4\02122007\J817483A.raw

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233 <210> SEQ ID NO: 5
234 <211> LENGTH: 2198
235 <212> TYPE: DNA
236 <213> ORGANISM: Zea mays
238 <220> FEATURE:
239 <221> NAME/KEY: promoter
240 <222> LOCATION: (1)...(2198)
241 <223> OTHER INFORMATION: ZmMADS
243 <400> SEQUENCE: 5
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246 ttacatgtcc ttcttctgct gttgctgctt gagcaggata tagagagatg accgacaccg 180
247 ggttgatctt gggacaacct tcttctcatc ttttcttcgt tgttttcttt tctattctca 240
248 ctaccttttt ctttctcttt gttcttccca ctggaggatt ctatcaaaaa gtattaccat 300
249 catacagagg aggaacccga agactatgaa ccatgtacaa cagtcttcaa cccaagaatc 360
250 accaagcatt gtgatcttag gggcgaggga gtggaaaaatg gagttgcttg tgatttggca 420
251 gaggggaattt tatcaggagt gttttgcttt gagtggaatg ggaactgagg gagttgttgg 480
252 gggggggggg tttataggcg agtgggagtg ctcggtgctg gagtgtggtg atggaacagg 540
253 tgacatgagg tagcaggctg atggaggggg gctgttgccg gcgatgatgg cggcgggtggg 600
254 tgcgctgcaa aggagggcgt ggggcggtgg tagtgcgcat ggaggcgggc acgcgtgcgg 660
255 ggggcacaag tgagtgggtg ggtcgatgac cctgatgttt gtggtctctg gttccaagaa 720
256 tctttgtctc tctttatgat aataacttct tttgtcgtcc ttttctgttt actttgactc 780
257 aggggcagtg ctttgattct cacggctcgt ctttttgact gagtgactgg acatgtttct 840
258 tctgtagcat tgtacaacat gtactttgtg caagctacaa ggccacattt tttgaagcat 900
259 agattctttc ccccaaaaaa tttatacaaa tatgcaaggc tacacttctt gtatttctat 960
260 aacattgtac attcatgaca gaggctcaaa agcttgtaaa ttttgtgcag gtttaattca 1020
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262 acacatgacc cccatgttat ttggtgacaa tacagaaacc acacatctag tgatgatata 1140
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270 accactatca atggacattt cacatagttt ccaagacttt gaaaacgggt tgacatgatt 1620
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272 cgtccaaaat gctgacgtga cataccatta aatgtgcatg aaactcccat aaaactttta 1740
273 ttgataatag cctcacagac atccggtcct acaccctgtg ggacccatca gccagacgcc 1800
274 ctgcagcaaa cgcgacgttt gacttgccat ctgctccct tgtgcccgcg cgaccctgga 1860
275 aggctggact ggaactggaa caagcaaaaat ggaaaaaacc atatctcacc actgaaccgc 1920
276 acccttcccg cccacgccag gctcgaccaa tcctgcccc gcgcgccttg acgagcgcat 1980
277 cactcgaacg ccggcctcgc taggcccata cttctggccc gcaataacga tccccgtcat 2040
278 gatccgacgg tctagctgcc tccacgccgc tccaaaaccc ccgcgtccaa tcaaaacacg 2100
279 acagcgggac gagcgaaacc accgtggttt cgccaaaccc ctttcttcc catctaaaac 2160
280 cgccccctcc cttcctcttc tctagctct cttgcctg 2198
282 <210> SEQ ID NO: 6
283 <211> LENGTH: 1470
284 <212> TYPE: DNA

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 02/12/2007  
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*KYI*  
Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:35; N Pos. 1366,1626,1629

## VERIFICATION SUMMARY

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L:1677 M:258 W: Mandatory Feature missing, &lt;220&gt; Tag not found for SEQ ID#:35

L:1700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:1320

M:341 Repeated in SeqNo=35